Figure 1

DSP-12, 1656 Base Pairs

```
AAGCAGTGGTAACAACGCAGAGTACGCGGGCGAGGAGAATATCTTGCTGGGAGTGGACT
TTTCCAGTAAGGAAAGTAAAAGCTGCACCATTGGG**ATG**GTTCTCCGACTGTGGAGCGAC
ACGAAAATCCACCTTGATGGAGATGGTGGGTTCAGCGTGAGCACAGCAGGAAGGATGCA
CATATTTAAGCCTGTGTCTGTCCAGGCCATGTGGTCTGCCCTGCAGGTGCTTCACAAGG
CCTGCGAAGTGGCCCGGAGGCACAACTACTTCCCCGGGGGTGTAGCTCTCATCTGGGCT
ACCTACTATGAGAGCTGCATCAGCTCCGAGCAGAGCTGCATCAACGAGTGGAACGCCAT
GCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCGCGCTATTTGTGGACAAGCCCACTG
AAGGGGAAAGGACCGAGCGCCTCATCAAAGCCAAGCTCCGAAGCATCATGATGAGCCAG
GATCTAGAAAATGTGACTTCCAAAGAGATTCGTAATGAATTAGAGAAACAGATGAATTG
TAACTTGAAGGAACTCAAGGAATTTATAGACAATGAGATGCTACTTATCTTGGGACAGA
TGGACAAGCCCTCCCTTATCTTCGATCATCTTTATCTCGGCTCTGAATGGAATGCATCC
AATCTGGAGGAACTGCAGGGCTCAGGGGTTGATTACATTTTAAATGTTACCAGAGAAAT
CGATAATTTTTTTCCTGGCTTATTTGCATATCATAACATCCGAGTCTACGATGAAGAGA
CCACAGACCTCCTCGCCCACTGGAATGAAGCGTATCATTTTATAAACAAAGCGAAGAGG
AACCATTCCAAGTGCCTGGTGCATTGCAAAATGGGCGTGAGTCGCTCGGCCTCCACAGT
CATAGCCTATGCAATGAAGGAATTCGGCTGGCCTCTGGAAAAAGCATATAACTATGTAA
AGCAGAAGCGCAGCATCACGCGCCCCAACGCGGGCTTTATGAGGCAGCTGTCTGAGTAT
GAAGGCATCTTGGATGCAAGCAAACAGCGGCACAACAAGCTGTGGCGTCAGCAGACAGA
CAGCAGCCTCCAGCAGCCTGTGGATGACCCTGCAGGACCTGGCGACTTCTTGCCAGAGA
CCCCAGATGGCACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCCAGCCCGGC
TTAGGGCCCCCCCTCCCCTGCTGTTTCCGGCGACTCTCAGACCCCCTTCTGCCTTCCCC
TGAGGATGAAGCCGGCAGCTTGGTCCACCTGGAGGATCCGGAGAGGGAGGCTCTGTTGG
AGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGGCCAGACAGCCCCAGCAAGGTTCC
GGACTCTGTGAGAAGGATGTGAAGAAGAAACTAGAGTTTGGGAGTCCCAAAGGTCGGAG
CGGCTCCTTGCTGCAGGTGGAGGAGACGGAAAGGGAGGAGGGCCTGGGAGCAGGGAGGT
GGGGGCAGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAACCTAAACAAC
AACAGCAAGAGGAGCTGTCCCAACGGCATGGAGGTAGGCAGAGCCCGGCCTGCAGGGTG
GCACACCCCATCCCTTCCATCCCACTCTAATTGGCCTACCTCAGCCTCTGTAGTAGGGA
CTACAGGCACCCGCCACCACACCCAGCTGATTTTTTTCTATTGTCTCCTCTGGGCCCCC
AGCTCCCATCTCCAGGGACCTGAGGGTTCTTTCACAGGG**TGA**TTCTGCTGGTGGGTACG
TAGTGCATACCTTATATAGCAAATTGAGAATCTGTTGGGAATAACACATATCTCTGCAC
ACCATCTTCACCCCATGTACCTTATTCATACCCTGGGCAGGGCTTCCAACTCAATTTCT
TTTTGTGTATGTAAAATTAAAACATATAATTTATCAGCCAAAAAAAAAAAAAAAAAAAA
AA
```

Figure 2

DSP-12, 552 Amino Acids

MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFP
GGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDSPALFVDKPTEGERTERLIKAK
LRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLY
LGSEWNASNLEELQGSGVDYILNVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAY
HFINKAKRNHSKCL**VHCKMGVSRS**ASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAG
FMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQLPF
LDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRP
ARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNL
LNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNWPTSASVVGTTGTRHHTQLIF
FYCLLWAPSSHLQGPEGSFTG

Figure 3

DSP-13, 1527 Base Pairs

CCTGGGAAGAAGTTATCTATCTCTCGAGTGACATTCAAGATATACCGTACCCCTCGGTTCTGTA
AGTCCTCTAAGTTGGAGGCATTCCATTCTGAGCCGGCCCC**ATG**ACCCTGAGCACGTTGGCCCGC
AAGAGGAAGGCGCCCCTCGCTTGCACCTGCAGCCTCGGTGGCCCCGACATGATTCCTTACTTCT
CCGCCAACGCGGTCATCTCGCAGAACGCCATCAACCAGCTCATCAGCGAGAGCTTTCTAACTGT
CAAAGGTGCTGCCCTTTTTCTACCACGGGGAAATGGCTCATCCACACCAAGAATCAGCCACAGA
CGGAACAAGCATGCAGGCGATCTCCAACAGCATCTCCAAGCAATGTTCATTTTACTCCGCCCAG
AAGACAACATCAGGCTGGCTGTAAGACTGGAAAGTACTTACCAGAATCGAACACGCTATATGGT
AGTGGTTTCAACTAATGGTAGACAAGACACTGAAGAAAGCATCGTCCTAGGAATGGATTTCTCC
TCTAATGACAGTAGCACTTGTACCATGGGCTTAGTTTTGCCTCTCTGGAGCGACACGCTAATTC
ATTTGGATGGTGATGGTGGGTTCAGTGTATCGACGGATAACAGAGTTCACATATTCAAACCTGT
ATCTGTGCAGGCAATGTGGTCTGCACTACAGAGCTTACACAAGGCTTGTGAAGTCGCCAGAGCG
CATAACTACTACCCAGGCAGCCTATTTCTCACTTGGGTGAGTTATTATGAGAGCCATATCAACT
CAGATCAATCCTCAGTCAATGAATGGAATGCAATGCAAGATGTACAGTCCCACCGGCCCGACTC
TCCAGCTCTCTTCACCGACATACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAA
TTAAGGGAGATCATGATGCAGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGT
TGGAAATGCAAATGGTGTGCAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGT
GATCCTTGGTCAAATGGATAGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGG
AATGCCTCCAACTTAGAGGACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAG
AGATAGATAACTTCTTCCCAGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGC
AACGGATCTCCTGGCGTACTGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGA
TCTAAATGCCTTGTGCACTGCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATG
CAATGAAGGAATATGGCTGGAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGT
AACCAAGCCCAACCCAAGCTTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGC
TTCCTAGGCTTGATTCATGGAGGGAGGGACAAGCCCTGGGGAGAGAAAGCACAGAATTTGAGT
CAGTAGATCTGGTTTCCATTCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACAT
TTCTCATCCTTACCTGACCCCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATT
GTGAATAAAAATGTGTTTGAATGTTTATAAAAAAAAAAAAAAAAAA

Figure 4

DSP-13, 509 Amino Acids

MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGS
STPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMVVVSTNGRQDTEES
IVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLH
KACEVARAHNYYPGSLFLTWVSYYESHINSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERER
TERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFE
HVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKF
ISKAKKHGSKCL**VHCKMGVSRS**ASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEE
YQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

Figure 5

A DSP13 Alternate Splice Variant, 723 Base Pairs

CTGCCCGGCTTCTAACAGGCCACTGACCGGTACTCACTGGGGACCCACGCTCTAAGTTGTTGAT
CTCTAGAACCGATTTTGGAAAAGGATTTGCCTTATTGAAGAAGACAGGATCATTCTTCTTTCTT
TCCCATTTAAGAATAATCGTTATTAAGAATATCGTTTAAGAATAATCGTTATTTCTCTCTTCTC
AGACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAATTAAGGGAGAT**CATG**ATGC
AGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGTTGGAAATGCAAATGGTGTG
CAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGTGATCCTTGGTCAAATGGAT
AGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGGAATGCCTCCAACTTAGAGG
ACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAGAGATAGATAACTTCTTCCC
AGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGCAACGGATCTCCTGGCGTAC
TGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGATCTAAATGCCTTGTGCACT
GCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATGCAATGAAGGAATATGGCTG
GAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGTAACCAAGCCCAACCCAAGC
TTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGCTTCCTAGGCTTGATTCATG
GAGGGAGGGACAAGCCCTGGGGAGAGAAAGCACAGAATTTGAGTCAGTAGATCTGGTTTCCAT
TCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACATTTCTCATCCTTACCTGACC
CCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATTGTGAATAAAAATGTGTTTG
AATGTTTATAAAAAAAAAAAAAAAAAAAA

B DSP13 Alternate Splice Variant, 241 Amino Acids

MMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASN
LEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL
VHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGL
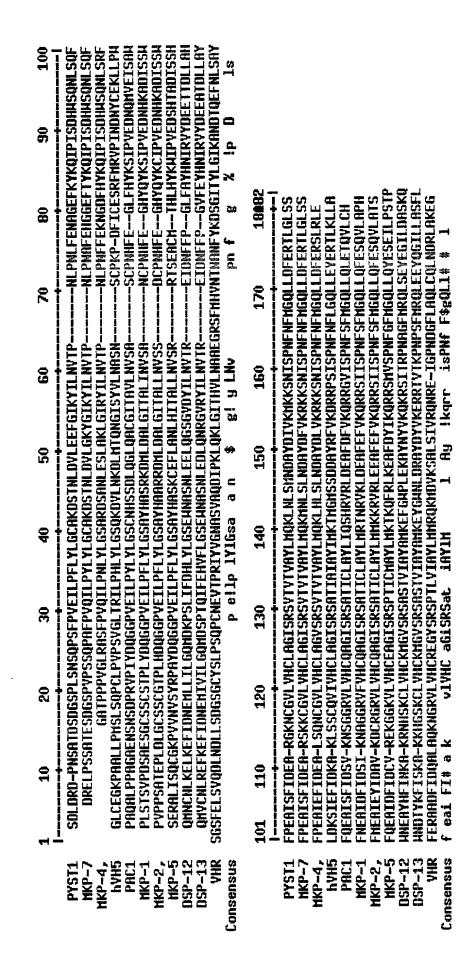IHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

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              1         10        20        30        40        50        60        70        80        90       100
              |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|
PYST1     SDLDRD-PNSATDSDGSPLSNSQPSFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTP-------NLPNLFENAGEFKYKQIPISDHHSQNLSQF
MKP-7     DRELPSSATESDGSPYPSSQPAFPVQILPYLYLGCAKDSTNLDVLGKYGIKYILNVTP-------NLPMAFEHGGEFTYKQIPISDHHSQNLSQF
MKP-4,    GATPPPYGLRASFPVQILPNLYLGSARDSANLESLAKLGIRYILNVTP-------NLPNFFEKNGDFHYKQIPISDHHSQNLSRF
hVH5      GLCEGKPAALLPHSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNASN-------SCPKP-DFICESRFMRVPINDNYCEKLLPH
PAC1      PAQALPPAGAENSNSDPRVPIYDQGGPVEILPYLYLGSCNHSSDLQGLQACGITAYLNVSA-------SCPMHFE--GLFHYKSIPVEDNQMVEISAH
MKP-1     PLSTSVPDSAESGCSSCSTPLYDQGGPVEILPYLYLGSAYHASRKDMLDALGITALINVSA-------NCPMHFE--GHYQYKSIPVEDNHKADISSA
MKP-2,    PVPPSATEPLDLGCSSCGTPLHDQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSS-------DCPMHFE--GHYQYKCIPVEDNHKADISSA
MKP-5     SERALISQCGKPVVNYSYRPAYDQGGPVEILPFLYLGSEANASMLEELQGSGVDYILNVSR-------RTSEACM--THLHYKAIPVEDSHTADISSH
DSP-12    QMNCNLKELKEFIDNEMLLILGQNDKPSLIFDHLYLGSEANASMLEDLQNRGVRYILNVTR-------EIDNFFP--GLFAYHNIRVYQEETTDLLAH
DSP-13    QMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEANASMLEDLQNRGVRYILNVTR-------EIDMFFP--GVFEYHNIRVYQDEEATDLLAY
VHR       SGSFELSVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAY
Consensus                      p ellp lYlGsa  a  n   $   gl y LMv        pn f  g   %  !p D    ls


            101  110       120       130       140       150       160       170      18082
              |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+--|
PYST1     FPEAISFIDEA-RGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSINDAYDIVKMKKSNISPNFNFMGQLLDFERTLGLSS
MKP-7     FPEAISFIDEA-RSKKCGVLVHCLAGISRSVTVTVAYLMQKMNLSLNDAYDFVKRKKSNISPNFNFMGQLLDFERTLGLSS
MKP-4,    FPEAIEFIDEA-LSQNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNFMGQLLDFERSLRLE
hVH5      LDKSIEFIDKA-KLSSCQVIVHCLAGISRSATIAIAYLMKTHGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYERTLKLLA
PAC1      FQEAISFIDSV-KNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFMGQLLQLETQVLCH
MKP-1     FNEAIDFIDSI-KNAGGRVFVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPH
MKP-2,    FNEAIEYIDAV-KDCRGRVLVHCQAGISRSATICLAYLMMKKRVRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLATS
MKP-5     FQEAIDFIDCV-REKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMVSPNFGFMGQLLQYESEILPSTP
DSP-12    HNEAYHFINKA-KRNHSKCLVHCKMGVSRSASTVIAYAMKEFGNPLEKAYNYVKQKRSIIRPNAGFNRQLSEYEGIIDASKQ
DSP-13    HNDTYKFISKA-KKHGSKCLVHCKMGVSRSASTVIAYAMKEYGNNLDRAYDYVKERRTVTKPNPSFNRQLEEYQGIILASFL
VHR       FERAADFIDQALAQKNGRVLVHCREGYSRSPTLVIAYLMMRQKMDVKSALSIVRQNRE-IGPNDGFLAQLCQLNDRLAKEG
Consensus f eal FI# a k   vlVHC aGiSRSat iAYlM   l  Ay !kqrr  isPNf F$gQLl#  # l
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Figure 6

Alignment of DSP-12 and DSP-13

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            10        20        30        40        50        60        70        80        90        100       110
         |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|

DSP-13   MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAYISQNAINQLISESFLTVKGAALFLPRGNGSSTPRISHRRNKHGDLQQHLQAHFILLRPEDNIRLAVRLESTYQNR


            120       130       140       150       160       170       180       190       200       210       220
         |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|

DSP-12                                                HVLRLHSDIKIIILDGDGGFSVSTNGRHIILFKPYSVQRHASALQVLIKACEVARRHNYFPGGVALIHATYYESCI
DSP-13   TRYHVYVYSTNGRQDTLESTVLGHDFSSNDSSTCTHGLVLPLHSDTLIIILDGDGGFSVSTDNRVHIFKPYSVQQHHSALQSLIHKACEVARHHNYYPGSLFLTHVSYYESHI


            230       240       250       260       270       280       290       300       310       320       330
         |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|

DSP-12   SSEQSCINEHNAHQUIESTRPDSPALFVDKPTEGERTERLIKAKLRSTHNSQDLENVTSKEIRNELEKQHNCNLKELKEFIDNEMLLILGQHDKPSLIFDHLYLGSEHHA
DSP-13   NSDQSSVNEHNAHQIVQSHRPDSPALFTDIPTERERTERLIKTKLREIHHQKDLENITSKEIRTELEMQHVCNLREFKEFIDNEMIVILGQHDSPTQIFEHVFLGSEHHA


            340       350       360       370       380       390       400       410       420       430       440
         |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|

DSP-12   SNLEELQGSGVDYIIHVTREIDNFFPGLFAYINIRYYDEETTDLLAHHHEAYIIFIHKAKRHIISKCLVICKHGVSRSASTVIAYAHKEFGHPLEKAYHYVKQKRSITRPNH
DSP-13   SNLEDLQNRGVRYILHVTREIDNFFPGVFEYHNIRYYDEEATDLLAYHHIYKFISKAKKHGSKCLVIICKHGVSRSASTVIAYAHKEYGHNLDRAYDYVKERRTVTKPHP


            450       460       470       480       490       500       510       520       530       540       550
         |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|

DSP-12   GFHRQLSEYEGILDHSKQR--HHKLHRQQTDSSLQ-QPVDDPAGPGDFLPETPDGTPESQLPFLDDHHQPGLGPPLPCCFRRLSDPLLPSPEDEHGSLVHLEDPEREALL
DSP-13   SFHRQLEEYUGILLISFLGLIHGGRDKPHGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK


            560       570       580       590       600       610       620       630       640       650       660
         |----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|----+----|

DSP-12   EEAPPAEVHRPARHJPQQGSGLCEKDVKKKLEFGSPKGRSGSLIQVEETEREEGLGAGRHGQLPTQLDQHLLNSEHLNNNSKRSCPHGHEVGRARPAGHHTPSLPSHSNH


            670       680       690       701
         |----+----|----+----|----+----|----+

DSP-12   PTSASVVGTIGTRHIITQLIFFYCLLHHPSSHLQGPEGSFTG
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Figure 7